



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/545,998

DATE: 07/28/2004

TIME: 14:14:16

Input Set : N:\CrF3\RULE60\09545998.raw
 Output Set: N:\CRF4\07282004\I545998.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Gorman, Daniel M.
 6 Randall, Troy D.
 7 Zlotnik, Albert

9 (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
 10 REAGENTS

12 (iii) NUMBER OF SEQUENCES: 8

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: DNAX Research Institute
 16 (B) STREET: 901 California Avenue
 17 (C) CITY: Palo Alto
 18 (D) STATE: California
 19 (E) COUNTRY: USA
 20 (F) ZIP: 94304-1104

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/545,998
 C--> 30 (B) FILING DATE: 10-Apr-2000
 W--> 35 (C) CLASSIFICATION: 536

C--> 40 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/911,423
 34 (B) FILING DATE: 14-AUG-1997
 37 (A) APPLICATION NUMBER: US 60/023,419
 38 (B) FILING DATE: 16-AUG-1996
 41 (A) APPLICATION NUMBER: US 60/027,901
 42 (B) FILING DATE: 07-OCT-1996

C--> 44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Ching, Edwin P.
 46 (B) REGISTRATION NUMBER: 34,090
 47 (C) REFERENCE/DOCKET NUMBER: DX0612K

C--> 49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 650-852-9196
 51 (B) TELEFAX: 650-496-1200

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:
 57 (A) LENGTH: 1073 base pairs
 58 (B) TYPE: nucleic acid
 59 (C) STRANDEDNESS: single

ENTERED

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60 (D) TOPOLOGY: linear
 62 (ii) MOLECULE TYPE: cDNA
 65 (ix) FEATURE:
 66 (A) NAME/KEY: CDS
 67 (B) LOCATION: 68..751
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 72 CTCGAGATCC ATTGTGCTGG AAAGGGAACT CCTGAAATCA GCCGACAGAA GACTCAGGAG 60
 74 AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT 109
 75 Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys
 76 1 5 10
 78 GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC 157
 79 Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly
 80 15 20 25 30
 82 CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC 205
 83 Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser
 84 35 40 45
 86 CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT 253
 87 Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys
 88 50 55 60
 90 GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG 301
 91 Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys
 92 65 70 75
 94 CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT 349
 95 His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile
 96 80 85 90
 98 GTG TTT GGC TTC CGG TGT GTT GCC TGT GGC ATG GGC ACC TTC TCC GCA 397
 99 Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala
 100 95 100 105 110
 102 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA 445
 103 Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
 104 115 120 125
 106 TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC 493
 107 Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
 108 130 135 140
 110 CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC 541
 111 Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
 112 145 150 155
 114 CTG GTC ATG GCT GCA TGC ATT TTC CTA ACC ACA GTC CAG CTC GGC 589
 115 Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
 116 160 165 170
 118 CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC 637
 119 Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
 120 175 180 185 190
 122 CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC 685
 123 Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
 124 195 200 205
 126 CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT 733
 127 Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
 128 210 215 220

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130	CTG	GGG	GGT	CGG	TGG	CCA	TGAGGCCTGG	TCTTCCTCTG	TGCCCAAGC	781										
131	Leu	Gly	Gly	Arg	Trp	Pro														
132	225																			
134	CAGACGCTAC	AAGACTTGCC	CAGCTATAACC	CTTGGTGAGA	GCAGGGGCCA	TGCTCTGCAC	841													
136	CCTTCCCTGG	GCCTGGCCCT	GCTCCCCCTCA	ACAGTGGCGG	AAGTGGGTGT	ATGAGAGCGG	901													
138	TGAGTTACGA	TTGGGCCCTA	TGGCTGCCTT	TCTCATTTGA	CAGCTCTGTT	GGAGTAGGGT	961													
140	CTTTGGGCC	ACCAAGAGCA	CCACGTTAG	CACAAGATCT	TGTACAAGAA	TAAATACTTG	1021													
142	TTTAGTAACC	TGAAAAAAA	AAAAAAAAGG	CGGGCCGCGG	AGGCCGAATT	CC	1073													
145	(2)	INFORMATION FOR SEQ ID NO: 2:																		
147	(i)	SEQUENCE CHARACTERISTICS:																		
148	(A)	LENGTH: 228 amino acids																		
149	(B)	TYPE: amino acid																		
150	(D)	TOPOLOGY: linear																		
152	(ii)	MOLECULE TYPE: protein																		
154	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:																		
156	Met	Gly	Ala	Trp	Ala	Met	Leu	Tyr	Gly	Val	Ser	Met	Leu	Cys	Val	Leu				
157	1					5				10							15			
159	Asp	Leu	Gly	Gln	Pro	Ser	Val	Val	Glu	Glu	Pro	Gly	Cys	Gly	Pro	Gly				
160						20				25							30			
162	Lys	Val	Gln	Asn	Gly	Ser	Gly	Asn	Asn	Thr	Arg	Cys	Cys	Ser	Leu	Tyr				
163						35				40							45			
165	Ala	Pro	Gly	Lys	Glu	Asp	Cys	Pro	Lys	Glu	Arg	Cys	Ile	Cys	Val	Thr				
166						50				55							60			
168	Pro	Glu	Tyr	His	Cys	Gly	Asp	Pro	Gln	Cys	Lys	Ile	Cys	Lys	His	Tyr				
169						65				70							75		80	
171	Pro	Cys	Gln	Pro	Gly	Gln	Arg	Val	Glu	Ser	Gln	Gly	Asp	Ile	Val	Phe				
172						85				90							95			
174	Gly	Phe	Arg	Cys	Val	Ala	Cys	Ala	Met	Gly	Thr	Phe	Ser	Ala	Gly	Arg				
175						100				105							110			
177	Asp	Gly	His	Cys	Arg	Leu	Trp	Thr	Asn	Cys	Ser	Gln	Phe	Gly	Phe	Leu				
178						115				120							125			
180	Thr	Met	Phe	Pro	Gly	Asn	Lys	Thr	His	Asn	Ala	Val	Cys	Ile	Pro	Glut				
181						130				135							140			
183	Pro	Leu	Pro	Thr	Glu	Gln	Tyr	Gly	His	Leu	Thr	Val	Ile	Phe	Leu	Val				
184						145				150							155		160	
186	Met	Ala	Ala	Cys	Ile	Phe	Phe	Leu	Thr	Thr	Val	Gln	Leu	Gly	Leu	His				
187						165				170							175			
189	Ile	Trp	Gln	Leu	Arg	Arg	Gln	His	Met	Cys	Pro	Arg	Glu	Thr	Gln	Pro				
190						180				185							190			
192	Phe	Ala	Glu	Val	Gln	Leu	Ser	Ala	Glu	Asp	Ala	Cys	Ser	Phe	Gln	Phe				
193						195				200							205			
195	Pro	Glu	Glu	Glu	Arg	Gly	Glu	Gln	Thr	Glu	Glu	Lys	Cys	His	Leu	Gly				
196						210				215							220			
198	Gly	Arg	Trp	Pro																
199	225																			
201	(2)	INFORMATION FOR SEQ ID NO: 3:																		
203	(i)	SEQUENCE CHARACTERISTICS:																		
204	(A)	LENGTH: 1006 base pairs																		
205	(B)	TYPE: nucleic acid																		

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206	(C) STRANDEDNESS: single	
207	(D) TOPOLOGY: linear	
209	(ii) MOLECULE TYPE: cDNA	
212	(ix) FEATURE:	
213	(A) NAME/KEY: CDS	
214	(B) LOCATION: 1..723	
217	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
219	ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG	48
220	Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu	
221	1 5 10 15	
223	GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC	96
224	Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro	
225	20 25 30	
227	GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC	144
228	Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg	
229	35 40 45	
231	TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG	192
232	Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu	
233	50 55 60	
235	GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC	240
236	Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His	
237	65 70 75 80	
239	TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA	288
240	Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro	
241	85 90 95	
243	GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT	336
244	Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys	
245	100 105 110	
247	ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC	384
248	Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys	
249	115 120 125	
251	AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT	432
252	Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro	
253	130 135 140	
255	GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA	480
256	Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala	
257	145 150 155 160	
259	GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC	528
260	Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Cys	
261	165 170 175	
263	GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG	576
264	Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu	
265	180 185 190	
267	AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG	624
268	Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val	
269	195 200 205	
271	CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG	672
272	Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu	
273	210 215 220	

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275 CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG	720
276 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp	
277 225 230 235 240	
279 GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG	773
280 Val	
283 GAGCTCCCCA GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGGCCCTG CTCCCTGGC	833
285 AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTCGGCGG	893
287 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT	953
289 GTCACCTAAA TTCAATTACAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA	1006

292 (2) INFORMATION FOR SEQ ID NO: 4:

294 (i) SEQUENCE CHARACTERISTICS:

295 (A) LENGTH: 241 amino acids
296 (B) TYPE: amino acid
297 (D) TOPOLOGY: linear

299 (ii) MOLECULE TYPE: protein

301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

303 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu	
304 1 5 10 15	
306 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro	
307 20 25 30	
309 Gly Cys Gly Pro Gly Arg Leu Leu Gly Thr Gly Thr Asp Ala Arg	
310 35 40 45	
312 Cys Cys Arg Val His Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu	
313 50 55 60	
315 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His	
316 65 70 75 80	
318 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro	
319 85 90 95	
321 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys	
322 100 105 110	
324 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys	
325 115 120 125	
327 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro	
328 130 135 140	
330 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala	
331 145 150 155 160	
333 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys	
334 165 170 175	
336 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu	
337 180 185 190	
339 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val	
340 195 200 205	
342 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu	
343 210 215 220	
345 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp	
346 225 230 235 240	

348 Val

351 (2) INFORMATION FOR SEQ ID NO: 5:

353 (i) SEQUENCE CHARACTERISTICS:

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09545998.raw

Output Set: N:\CRF4\07282004\I545998.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:36 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:40 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:44 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:49 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]